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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/993,808	11/06/2001	William J. Gordon-Kamm	1146	8538

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EXAMINER	
COLLINS, CYNTHIA E	

ART UNIT	PAPER NUMBER
1638	

DATE MAILED: 10/26/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/993,808	GORDON-KAMM ET AL.	
	Examiner	Art Unit	
	Cynthia Collins	1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *June 29, 2004*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-78* is/are pending in the application.

4a) Of the above claim(s) *12 and 14-78* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1,3-11 and 13* is/are rejected.

7)☒ Claim(s) *2* is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *2/02,12/03,5/04*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

Election/Restrictions

Applicant's election with traverse of Group I, claims 1-11 and 13, and SEQ ID NO:1, in the reply filed on June 29, 2004 is acknowledged. The traversal is on the ground(s) that the isolated nucleic acids and the methods of use are sufficiently related so as to be examined in one application without imposing an undue burden. Applicants specifically point out that SEQ ID NOS: 1 and 5 are closely related in that the nucleic acid represented in groups (A) (SEQ ID NO: 1) has 89.9% identity to the nucleic acid represented by groups (C) (SEQ ID NO: 5), and in that the sequences also contain a conserved domain. Applicants therefore submit that groups (A) and (C) are closely related so as to be combined without undue burden. This is not found persuasive because SEQ ID NOS: 1 and 5 comprise different nucleic acid sequences and encode different amino acid sequences. Accordingly the sequences must be separately searched.

The requirement is still deemed proper and is therefore made FINAL. Claims 12 and 14-78, and the nonelected sequences, are withdrawn from consideration as being directed to nonelected inventions.

Information Disclosure Statement

Initialed and dated copies of Applicant's IDS form 1449, filed February 12, 2002, December 19, 2003 and May 17, 2004 are attached to the instant Office action.

Specification

The specification is objected to for failing to comply with 37 CFR 1.821 in that sequences recited in the text are not referred to by use of a sequence identifier preceded by "SEQ ID NO:", for example at page 49 lines 17-23. Appropriate correction is required.

Claim Objections

Claim 1 is objected to for failing to comply with 37 CFR 1.821 in that sequences recited in the claim are not referred to by use of a sequence identifier preceded by "SEQ ID NO:" Appropriate correction is required.

Claim 1 is objected to for reciting the undefined acronyms CDK and CKI. Appropriate correction is required.

Claim 13 is objected to for depending on a withdrawn claim. Appropriate correction is required.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 1, 3-11 and 13 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the

relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Claim 1 is drawn to an isolated nucleic acid comprising a) a polynucleotide that encodes a polypeptide of SEQ ID NO: 2, b) a polynucleotide of unspecified structure and function amplified from a *Zea mays* nucleic acid library using primers from SEQ ID NO: 1, c) a polynucleotide of unspecified structure and function amplified from a *Zea mays* nucleic acid library using a 5' primer comprising ATG GGN MR TAY ATG (CGN or AGR) MR and a 3' primer comprising SEQ ID NO: 1, d) a polynucleotide of unspecified structure and function amplified from a *Zea mays* nucleic acid library using a 5' primer comprising ATG GGN MR TAY ATG (CGN or AGR) MR and a 3' primer comprising the CDK binding region of SEQ ID NO: 1, e) a polynucleotide of unspecified function comprising at least 20 contiguous bases of SEQ ID NO: 1, f) a polynucleotide of unspecified function comprising at least 20 contiguous bases of SEQ ID NO: 1 and ATG GGN MR TAY ATG (CGN or AGR) MR, g) a polynucleotide of unspecified function comprising at least 20 contiguous bases of the 3' coding region of SEQ ID NO: 1, h) a polynucleotide of unspecified function comprising at least 20 contiguous bases of the 3' coding region of SEQ ID NO: 1 and at least some of the CDK binding region, i) a polynucleotide of unspecified structure encoding a maize CKI protein, j) a polynucleotide of unspecified function having at least 82% sequence identity to SEQ ID NO:1, k) a polynucleotide of unspecified structure and function at least 25 nucleotides in length which hybridizes under low stringency conditions to a polynucleotide having the sequence set forth in SEQ ID NO: 1, l) a polynucleotide of unspecified structure and function at least 25 nucleotides in length that is a coding sequence which hybridizes under low stringency conditions to a polynucleotide having

the sequence set forth in SEQ ID NO: 1, and p) a polynucleotide complementary to a polynucleotide of (a) through (l). Claims 3-11 and 13 are drawn to the isolated nucleic acid of claim 1 adducted to a second nucleic acid sequence encoding a DNA-binding domain, a vector comprising at least one nucleic acid of claim 1, an expression cassette comprising at least one nucleic acid of claim 1 operably linked to a promoter wherein the nucleic acid is in sense or antisense orientation, a host cell containing at least one expression cassette of claim 5, a transgenic plant comprising at least one expression cassette of claim 5, seed from the transgenic plant of claim 8, and a ribonucleic acid sequence encoding a protein of claim 12.

The specification describes a single polynucleotide encoding a maize CKI protein that inhibits kinase activity, a polynucleotide comprising the 1372 base pair nucleotide sequence of SEQ ID NO:1 encoding a polypeptide comprising the 256 amino acid sequence of SEQ ID NO:2 (pages 48-49; sequence listing). The specification does not describe other polynucleotides comprising other nucleotide sequences encoding polypeptides that inhibit kinase activity, or other polynucleotides comprising other nucleotide sequences that are functional subfragments of SEQ ID NO:1 or structural and/or functional variants of SEQ ID NO:1.

The Federal Circuit has recently clarified the application of the written description requirement. The court stated that "A description of a genus of cDNAs may be achieved by means of recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to members of the genus, which features constitute a substantial portion of the genus." See *University of California v. Eli Lilly and Co.*, 119 F.3d 1559, 1569; 43 USPQ2d 1398, 1406 (Fed. Cir. 1997).

In the instant case Applicant has not described a representative number of species falling within the scope of the claimed genus which encompasses numerous undisclosed functional subfragments of SEQ ID NO:1 and structural and/or functional variants of SEQ ID NO:1, nor the structural features unique to the genus.

Claims 1, 3-11 and 13 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for an isolated nucleic acid comprising a polynucleotide that encodes a polypeptide of SEQ ID NO: 2, as well as an expression cassette comprising a polynucleotide that encodes a polypeptide of SEQ ID NO: 2 operably linked to a promoter wherein the nucleic acid is in a sense orientation, a host cell and transgenic plant and seed comprising said expression cassette, does not reasonably provide enablement for other polynucleotide sequences, or for expression cassettes comprising a polynucleotide that encodes a polypeptide of SEQ ID NO: 2 operably linked to a promoter wherein the nucleic acid is in an antisense orientation. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims.

Claim 1 is drawn to an isolated nucleic acid comprising a) a polynucleotide that encodes a polypeptide of SEQ ID NO: 2, b) a polynucleotide of unspecified structure and function amplified from a *Zea mays* nucleic acid library using primers from SEQ ID NO: 1, c) a polynucleotide of unspecified structure and function amplified from a *Zea mays* nucleic acid library using a 5' primer comprising ATG GGN MR TAY ATG (CGN or AGR) MR and a 3' primer comprising SEQ ID NO: 1, d) a polynucleotide of unspecified structure and function

amplified from a *Zea mays* nucleic acid library using a 5' primer comprising ATG GGN MR TAY ATG (CGN or AGR) MR and a 3' primer comprising the CDK binding region of SEQ ID NO: 1, e) a polynucleotide of unspecified function comprising at least 20 contiguous bases of SEQ ID NO: 1, f) a polynucleotide of unspecified function comprising at least 20 contiguous bases of SEQ ID NO: 1 and ATG GGN MR TAY ATG (CGN or AGR) MR, g) a polynucleotide of unspecified function comprising at least 20 contiguous bases of the 3' coding region of SEQ ID NO: 1, h) a polynucleotide of unspecified function comprising at least 20 contiguous bases of the 3' coding region of SEQ ID NO: 1 and at least some of the CDK binding region, i) a polynucleotide of unspecified structure encoding a maize CKI protein, j) a polynucleotide of unspecified function having at least 82% sequence identity to SEQ ID NO:1, k) a polynucleotide of unspecified structure and function at least 25 nucleotides in length which hybridizes under low stringency conditions to a polynucleotide having the sequence set forth in SEQ ID NO: 1, l) a polynucleotide of unspecified structure and function at least 25 nucleotides in length that is a coding sequence which hybridizes under low stringency conditions to a polynucleotide having the sequence set forth in SEQ ID NO: 1, and p) a polynucleotide complementary to a polynucleotide of (a) through (l). Claims 3-11 and 13 are drawn to the isolated nucleic acid of claim 1 adducted to a second nucleic acid sequence encoding a DNA-binding domain, a vector comprising at least one nucleic acid of claim 1, an expression cassette comprising at least one nucleic acid of claim 1 operably linked to a promoter wherein the nucleic acid is in sense or antisense orientation, a host cell containing at least one expression cassette of claim 5, a transgenic plant comprising at least one expression cassette of claim 5, seed from the transgenic plant of claim 8, and a ribonucleic acid sequence encoding a protein of claim 12.

The specification discloses the isolation of a single polynucleotide encoding a maize CKI protein that inhibits kinase activity, a polynucleotide comprising the 1372 base pair nucleotide sequence of SEQ ID NO:1 encoding a polypeptide comprising the 256 amino acid sequence of SEQ ID NO:2 (pages 48-49; sequence listing). The specification also discloses an expression cassette comprising said polynucleotide operably linked to a promoter wherein the nucleic acid is in sense orientation, a bacterial host cell containing said expression cassette, and expression of the encoded maize CKI protein in said host cell (page 48). The specification does not disclose how to make and use other polynucleotides comprising other nucleotide sequences that encode polypeptides that inhibit kinase activity, or how to make and use other polynucleotides comprising other nucleotide sequences that are functional subfragments of SEQ ID NO:1 or structural and/or functional variants of SEQ ID NO:1, or how to make and use an expression cassette comprising SEQ ID NO:1 or its subfragments or variants operably linked to a promoter wherein the nucleic acid is in antisense orientation.

The full scope of the claimed invention is not enabled because the functionality of variants or fragments of SEQ ID NO:1 is unpredictable, since structurally homologous amino acid sequences are not always functionally homologous.

See, for example, Broun P et al. (Catalytic plasticity of fatty acid modification enzymes underlying chemical diversity of plant lipids. Science. 1998 Nov 13;282(5392):1315-7), who teach that a *Lesquerella fendleri* oleate hydroxylase having 81% sequence identity to an *Arabidopsis thaliana* oleate desaturase has only 71 % sequence identity to *Ricinus communis* oleate hydroxylase (page 1315 column 2 first full paragraph). Broun et al. also teach that as few

as four amino acid substitutions can change an oleate 12-desaturase to a hydroxylase (paragraph spanning pages 1316-1317).

See also, for example, Zhou et al. (Plant J. 2003 Aug;35(4):476-89), who teach that expression of an N-terminal truncation of an *Arabidopsis* CKI increases CKI effects on transgenic plants, whereas expression of a C-terminal truncation of the *Arabidopsis* CKI greatly reduces or abolishes CKI effects on transgenic plants, as compared to control plants expressing the full-length CKI protein (page 476 Abstract; page 479 Figure 2; page 480 Table 1).

In the instant case the specification does not provide sufficient guidance with respect to which structural elements of SEQ ID NO:1 would be retained by variants or fragments thereof that function in the same manner as SEQ ID NO:1, or whose specific function differs from that of SEQ ID NO:1. Absent such guidance one skilled in the art would have to isolate and or synthesize numerous different subfragments or sequence variants, and then test each subfragment or sequence variant for specific functions associated with CKI coding sequences in order to discriminate between functional and nonfunctional subfragments and variants, and in order to assign specific functions to functional subfragments and variants. Such a trial and error approach to practicing the claimed invention would constitute undue experimentation.

The claimed invention is also not enabled because making and using antisense expression cassettes is unpredictable, as the ability of an antisense transcript to suppress gene expression depends on multiple variables which include but are not limited to the length of the antisense transcript, its position relative to the parent gene, and the degree of homology between the antisense transcript and the gene to be suppressed.

See, for example, Sandler et al. (Inhibition Of Gene Expression In Transformed Plants By Antisense RNA. Plant Molecular Biology, 1988, Vol. 11, No. 3, pages 301-310), who teach that DNA fragments encoding different portions of the nopaline synthase gene, when expressed as antisense transcripts, vary in their ability to inhibit nopaline synthase gene expression (page 308 column 2 and Table 4, page 309 column 1 first full paragraph). Antisense transcripts downstream from the Cla I site (nucleotide 373) effectively suppressed nopaline synthase gene expression, whereas the full length antisense transcript and the antisense transcript upstream from the Cla I site (nucleotides 1 to 373) did not (id).

See also, for example, van der Krol AR et al. (Inhibition of flower pigmentation by antisense CHS genes: promoter and minimal sequence requirements for the antisense effect. Plant Mol Biol. 1990 Apr;14(4):457-66), who teach a method of decreasing the expression of an endogenous petunia chalcone synthase gene by transforming petunia cells with chimeric genes comprising chalcone synthase (CHS) coding sequences operably linked in an antisense orientation to a CaMV 35S constitutive promoter. The full length CHS cDNA and CHS sequences encoding half-length or quarter-length RNA complementary to the 3' half of the CHS mRNA decreased the expression of endogenous CHS, whereas half-length RNA complementary to the 5' half of the CHS mRNA did not (page 460 Figures 1 and 2;page 461 Figure 3).

See additionally, for example, Waterhouse PM et al. (Virus resistance and gene silencing: killing the messenger. Trends in Plant Science, November 1999, Vol. 4, No. 11, pages 452-457), who teach that antisense suppression of gene expression requires a high degree of sequence homology (>75%) between the endogenous sequence and the antisense transgene to be effective (page 453 column 1 second full paragraph).

In the instant case the specification does not provide sufficient guidance with respect to how to make and use antisense expression cassettes that function in a specific manner. Absent such guidance one skilled in the art would have to test each of the myriad sequences encompassed by the claims for its specific effect on a host cell or plant transformed therewith in order to discriminate between functional and nonfunctional subfragments and variants, and in order to assign specific functions to functional subfragments and variants. Such a trial and error approach to practicing the claimed invention would constitute undue experimentation.

Claim Rejections - 35 USC § 101

Claims 10-11 are rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter.

Claims 10-11 are drawn to seed, but are not limited to seed that comprise the construct that was introduced into the parent plant. Due to Mendelian inheritance of genes, a single construct introduced into the parent plant would only be transferred to half of the seeds of that plant. In addition, given that there is no indication that there are any other distinguishable characteristics of the claimed seed, the claimed seed are not distinguishable from seed that occur in nature. See *Diamond v. Chakrabarty,* 447 U.S. 303 (1980), *Funk Bros. Seed Co. V. Kalo Inoculant Co.*, 233 U.S. 127 (1948), and *In re Bergey*, 195 USPQ 344, (CCPA). The amendment of the claims to indicate that the claimed seed comprise the expression cassette that was introduced into their parent plant would overcome the rejection.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 1, 4-9 and 13 are rejected under 35 U.S.C. 102(b) as being anticipated by Klein et al. (WO 00/60087, published 12 October 2000, Applicant's IDS).

Claim 1 is drawn to maize CKI sequences, including an isolated nucleic acid comprising a polynucleotide amplified from a *Zea mays* nucleic acid library using primers from SEQ ID NO: 1, a polynucleotide comprising at least 20 contiguous bases of SEQ ID NO: 1, a polynucleotide comprising at least 20 contiguous bases of the 3' coding region of SEQ ID NO: 1, a polynucleotide encoding a maize CKI protein, and a polynucleotide at least 25 nucleotides in length that is a coding sequence which hybridizes under low stringency conditions to a polynucleotide having the sequence set forth in SEQ ID NO: 1. Claims 4-9 and 13 are drawn to a vector comprising at least one nucleic acid of claim 1, an expression cassette comprising at least one nucleic acid of claim 1 operably linked to a promoter wherein the nucleic acid is in sense or antisense orientation, a host cell containing at least one expression cassette of claim 5, a transgenic plant including corn and soybean comprising at least one expression cassette of claim 5, and a ribonucleic acid sequence encoding a protein of claim 12.

Klein et al. teach maize CKI sequences, including a polynucleotide comprising at least 20 contiguous bases of SEQ ID NO: 1, a polynucleotide comprising at least 20 contiguous bases of the 3' coding region of SEQ ID NO: 1, and a polynucleotide encoding a maize CKI protein

(pages 22-24; Figure 1; SEQ ID NOS:1, 2, 3; attached sequence alignments). The maize CKI sequences taught by Klein et al. could be amplified from a *Zea mays* nucleic acid library using primers from SEQ ID NO: 1 and would hybridize under low stringency conditions to a polynucleotide having the sequence set forth in SEQ ID NO: 1 due to the high degree of sequence similarity between SEQ ID NO:1 and the maize CKI sequences taught by Klein et al. (see attached sequence alignment). Klein et al. also teach a vector, expression cassettes comprising a nucleic acid operably linked to a promoter wherein the nucleic acid is in sense or antisense orientation, host cells and transgenic plants including corn and soybean, and ribonucleic acids (page 2 line 29 to page 3 line 2; page 7 lines 20-23; page 11 lines 29-30; page 12 lines 13-21; page 15 line 33 to page 17 line 31; pages 25-28).

Claims 10-11 are rejected under 35 U.S.C. 102(b) as being anticipated by Barcelo P et al. (Transgenic cereal (tritordeum) plants obtained at high efficiency by microprojectile bombardment of inflorescence tissue. Plant J. 1994 Apr;5(4):583-92).

The claims are drawn to seed from the transgenic plant of claim 8, including a barley plant.

Barcelo et al. teach seed from transgenic barley plants (page 586 column 2 first full paragraph; page 589 column 2 second full paragraph). While Barcelo et al. do not teach seed from the transgenic plant of claim 8, Barcelo et al. need not teach the transgenic plant of claim 8 as the source of their seed to anticipate the claimed seed. Due to Mendelian inheritance of genes, a single construct introduced into the parent plant would only be transferred to half of the seeds of that plant. In addition, given that there is no indication that there are any other distinguishable

characteristics of the claimed seed, the claimed seed are not distinguishable from seed that occur in nature. The amendment of the claims to indicate that the claimed seed comprise the expression cassette that was introduced into their parent plant would overcome the rejection.

Allowable Subject Matter

Claim 2 is objected to as being dependent upon a rejected base claim, but would be allowable if rewritten in independent form and limited to SEQ ID NO:1.

Remarks

No claim is allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Cynthia Collins whose telephone number is (571) 272-0794. The examiner can normally be reached on Monday-Friday 8:45 AM -5:15 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Amy Nelson can be reached on (571) 272-0804. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Cynthia Collins Cynthia Collins 10/22/04